

### SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (ii) TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT OF THROMBOSIS
- (iii) NUMBER OF SEQUENCES: 111
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: SmithKline Beecham Corporation
  - (B) STREET: 709 Swedeland Road
  - (C) CITY: King of Prussia
  - (D) STATE: PA
  - (E) COUNTRY: USA
  - (F) ZIP: 19406
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 09/346,487
  - (B) FILING DATE: 01-JUL-1999
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/783,853
  - (B) FILING DATE: 16-JAN-1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Baumeister, Kirk
  - (B) REGISTRATION NUMBER: 33,833
  - (C) REFERENCE/DOCKET NUMBER: P50438-1



- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 610-270-5096
  - (B) TELEFAX:
  - (C) TELEX:
  - (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

# CATCCTAGAG TCACCGAGGA

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- (2) INFORMATION FOR SEQ ID NO:2:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

## AGCTGCCCAA AGTGCCCAAG C

21

(2) INFORMATION FOR SEQ ID NO:3:



(i)	SEQUENCE	CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

# CTAACACTCA TTCCTGTTGA AGCTCTTGAC AATGGG

36

- (2) INFORMATION FOR SEQ ID NO:4:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

# GATTTTCARG TGCAGATTTT C

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- (2) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 363 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO





- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAGATCCAGT	TGGTGCAGTC	TGGACCTGAG	CTGAAGAAGC	CTGGAGAGAC	AGTCAAGATC	60
TCCTGCAAGG	${\tt CTTCTGGGTA}$	CACCTTCACA	AACTATGGAA	TGAACTGGGT	GAAGCAGGCT	120
CCAGGAAAGG	${\tt GTTTAAAGTG}$	${\tt GATGGGCTGG}$	ATAAACACCA	GAAATGGAAA	GTCAACATAT	180
GTTGATGACT	${\tt TCAAGGGACG}$	${\tt GTTTGCCTTC}$	TCTTTGGAAA	GCTCTGCCAG	CACTGCCAAT	240
TTGCAGATCG	ACAACCTCAA	AGATGAGGAC	ACGGCTACAT	ATTTCTGTAC	AAGAGAAGGG	300
AATATGGATG	GTTACTTCCC	${\bf T}{\bf T}{\bf T}{\bf T}{\bf A}{\bf C}{\bf T}{\bf T}{\bf A}{\bf C}$	TGGGGCCAAG	GGACTCTGGT	CACTGTCTCT	360
GCA						363

### (2) INFORMATION FOR SEQ ID NO:6:

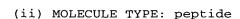
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 321 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAAATTGTTC	TCTCCCAGTC	TCCAGCAATC	CTGTCTGCAT	CTCCAGGGGA	GAAGGTCACA	60
ATGACTTGCA	GGGCCAGCTC	AAGTGTAAAT	TACATGCACT	GGTACCAGCA	GAAGCCAGGA	120
TCCTCCCCA	AACCCTGGAT	TTATGCCACA	TCCAACCTGG	CTTCTGGAGT	CCCTGCTCGC	180
TTCAGTGGCA	$\tt GTGGGTCTGG$	${\tt GACCTCTTAC}$	TCTCTCACAA	TCAGCAGAGT	GGAGGCTGAA	240
GATGCTGCCA	${\tt CTTATTACTG}$	${\tt CCAGCAGTGG}$	AGTATTAACC	CACGGACGTT	CGGTGGAGGC	300
ACCAAGCTGG	AAATCAAACG	G				321

### (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 121 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear



- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr 20 25 Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met 40 Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Ser Ser Ala Ser Thr Ala Asn 70 75 Leu Gln Ile Asp Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys 90 Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly 100 105 110 Gln Gly Thr Leu Val Thr Val Ser Ala

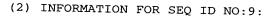
120

### (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asn Tyr Gly Met Asn 1 5

115



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr

1 5 10

- (2) INFORMATION FOR SEQ ID NO:11:
- (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly

1 5 10 15

Glu Ivs Val Thr Met Thr Cvs Avy Ala Ser Pro Gly

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr 35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr 85 90 95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

- (2) INFORMATION FOR SEQ ID NO:12:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg Ala Ser Ser Ser Val Asn Tyr Met His
1 5 10

- (2) INFORMATION FOR SEQ ID NO:13:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala Thr Ser Asn Leu Ala Ser

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- (2) INFORMATION FOR SEQ ID NO:14:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gln Gln Trp Ser Ile Asn Pro Arg Thr
1 5

- (2) INFORMATION FOR SEQ ID NO:15:
- (i) SEQUENCE CHARACTERISTICS:



,		
(A)	LENGTH: 104 base	pairs
(B)	TYPE: nucleic aci	id
(C)	STRANDEDNESS: sir	ngle
(D)	TOPOLOGY: linear	
(ii) M	OLECULE TYPE: cDi	ΙA
(iii)	HYPOTHETICAL: NO	
(iv) A	NTISENSE: NO	

(v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CAACTAGTGC AATCTGGGTC TGAGTTGAAG AAGCCTGGGG CCTCAGTGAA GGTTTCCTGC 60 AAGGCCTCTG GATACACCTT CACTAACTAT GGAATGAACT GGGT 104

(2) INFORMATION FOR SEQ ID NO:16:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTGAAGTCAT CAACATATGT TGACTTTCCA TTTCTGGTGT TTATCCATCC CATCCACTCG 60 AGCCCTTGTC CAGGGGCCTG TCGCACCCAG TTCATTCCAT AGTTAGTG 108

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 107 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA



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(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
GTCAACATAT GTTGATGACT TCAAGGGGCG GTTTGTCTTC CCTCTGTCAG CACGGCATAT	60
CTACAGATCA GCAGCCTAAA GGCTGACGAC ACTGCAGTGT ATTACTG	107
(2) INFORMATION FOR SEQ ID NO:18:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 91 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
GGTACCCTGG CCCCAGTAAG TAAAAGGGAA GTAACCATCC ATATTCCCTT CTCTCGCACA	60
GTAATACACT GCAGTGTCGT CAGCCTTTAG G	91

- (2) INFORMATION FOR SEQ ID NO:19:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 337 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:





- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 2...337
- (D) OTHER INFORMATION:

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

A C	TA C	FTG (	CAA 1	CT G	GG I	CT C	SAG 7	TG A	AAG A	AG C	CT (	GGG (	GCC T	гса с	GTG AAG	49
Ι	eu V	al (	3ln S	Ser G	ly S	er G	lu I	eu I	ys I	ys F	ro (	Gly A	Ala S	Ser V	al Lys	
	1				5					.0					.5	
GTI	TCC	TGC	C AAG	GCC	TCT	GGA	TAC	ACC	TTC	ACT	' AA(	C TAT	GGA	ATC	AAC	97
Val	Ser	Суз	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asr	і Туг	Gly	Met	Asn	<i>J i</i>
			20					25					30			
TGG	GTG	CGA	CAG	GCC	ССТ	GGA	CAA	GGG	СТС	GAG	TGG	ATG	GGA	TGG	ATA	145
Trp	Val		Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Trp	Ile	
		35					40					45				
AAC	ACC	AGA	ААТ	GGA	AAG	TCA	ACA	TAT	GTT	GAT	GAC	TTC	AAG	GGG	CGG	193
Asn	Thr	Arg	Asn	Gly	Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe	Lys	Gly	Arg	
	50					55					60		_	-	J	
TTT	GTC	TTC	TCC	TTG	GAC	ACC	TCT	GTC	AGC	ACG	GCA	TAT	СТА	CAG	ATC	241
Phe	Val	Phe	Ser	Leu	Asp	Thr	Ser	Val	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	241
65					70					75					80	
AGC	AGC	СТА	AAG	GCT	GAC	GAC	ACT	GCA	GTG	TAT	TAC	TGT	GCG	AGA	GAA	289
				Ala												205
				85					90					95		
GGG	ААТ	ATG	GAT	GGT	TAC	TTC	CCT	TTT	АСТ	TAC	TGG	GGC	CAG	GGT	ACC	337
Gly	Asn	Met	Asp	Gly	Tyr	Phe	Pro	Phe	Thr	Tyr	Trp	Gly	Gln	Gly	Thr	337
			100					105			_	-	110	-4	<del>-</del>	

# (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear





- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

 Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala Ser Val Lys

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 Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn 20
 25
 30

 Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile 35
 40
 45

 Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg 50
 55
 60

Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln Ile 65 70 75 80

Ser Ser Leu Lys Ala Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu 85 90 95

Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr
100 105 110

- (2) INFORMATION FOR SEQ ID NO:21:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCTACTAGTG CAATCTGGGT CTGAGTTGAA GCC

(2) INFORMATION FOR SEQ ID NO:22:

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(i) SEQUENCE CHARACTERISTICS:





- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

#### TGGGTACCCT GGCCCCAGTA AGTAAAAGGG

30

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- (2) INFORMATION FOR SEQ ID NO:23:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 97 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 27...95
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC

Met Gly Trp Ser Cys Ile Ile Leu Phe 5

TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC CAG GTC CAA CTA GT Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Val Gln Leu 10 20

97

- (2) INFORMATION FOR SEQ ID NO:24:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1 5 10 15

Val His Ser Gln Val Gln Leu
20

- (2) INFORMATION FOR SEQ ID NO:25:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 110 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:



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# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGAGACGCCA TCGAATTCTG AGCACACAGG ACCTCACCAT GGGATGGAGC TGTATCATCC 60
TCTTCTTGGT AGCAACAGCT ACAGGTGTCC ACTCCCAGGT CCAACTGCAG 110

# (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

# GGAGACGCCA TCGAATTCTG A

21

- (2) INFORMATION FOR SEQ ID NO:27:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GATTGCACTA GTTGGACCTG GGAGTGGACA

30



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<ol><li>INFORMATION</li></ol>	FOR	SEQ	ID	NO:28:
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(i)	SEQUENCE	CHARACTERISTICS

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTAGAGTGGG	TCGCAGAGAT	CTCTGATGGT	GGTAGTTACA	CCTACTATCC	AGACACTGTG	60
ACGGGCCGGT						77

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 73 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATCGTGAACC GGCCCGTCAC AGTGTCTGGA TAGTAGGTGT AACTACCACC ATCAGAGATC

73

- (2) INFORMATION FOR SEQ ID NO:30:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 363 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single



### (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...363
  - (D) OTHER INFORMATION: F9HZHC 1-0

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAG	GTG	CAA	СТА	GTG	CAA	TCT	GGG	TCI	GAG	TTG	AAG	. AAG	CCI	' GGG	GCC	48
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ser	Glu	Leu	Lys	Lys	Pro	Gly	Ala	
1				5					10					15		
TCA	GTG	AAG	GTT	TCC	TGC	AAG	GCC	TCT	GGA	TAC	ACC	TTC	ACT	AAC	TAT	96
Ser	Val	Lys		Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	
			20					25					30			
GGA	ΔͲር	<u>አ</u> አር	TICC	СТС	CCA	07.0	000									
Glv	Met	Agn	TGG	Ua1	CGA	CAG	GCC	CCT	GGA	CAA	GGG	CTC	GAG	TGG	ATG	144
011	1100	35	Trp	vai	Arg	GIII	40	Pro	GIY	GIn	Gly		Glu	Trp	Met	
		-					40					45				
GGA	TGG	АТА	AAC	ACC	AGA	ААТ	GGA	AAG	ጥሮል	ΔCΔ	ጥለጥ	Cmm	Cam	G 3 G	mm c	4.0.0
Gly	Trp	Ile	Asn	Thr	Arq	Asn	Glv	Lvs	Ser	Thr	TAL	Ual	Aan	GAC 7 an	TTC	192
	50					55	1	_10	DCI	1111	60	vai	Asp	Asp	Pne	
AAG	GGA	CGG	TTT	GTC	TTC	TCC	TTG	GAC	ACC	TCT	GTC	AGC	ACG	GCA	тат	240
Lys	Gly	Arg	Phe	Val	Phe	Ser	Leu	Asp	Thr	Ser	Val	Ser	Thr	Ala	Tvr	240
65					70					75					80	
CTA	CAG	ATC	AGC	AGC	CTA	AAG	GCT	GAC	GAC	ACT	GCA	GTG	ТАТ	TAC	TGT	288
Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		
~~~																
GCG	AGA -	GAA	GGG	AAT	ATG	GAT	GGT	TAC	TTC	CCT	TTT	ACT	TAC	TGG	GGC	336
Ala	Arg			Asn	Met	Asp	Gly	Tyr	Phe	Pro	Phe	Thr	Tyr	Trp	Gly	
			100					105					110			



CAG GGT ACC CTG GTC ACC GTC TCA
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

### (2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 121 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
- Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala 10 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr 25 2.0 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met 40 Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe 60 55 Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr 75 70 Leu Gln Ile Ser Ser Leu Lys Ala Asp Asp Thr Ala Val Tyr Tyr Cys 90 Ala Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly 105 100 Gln Gly Thr Leu Val Thr Val Ser Ser 120 115
- (2) INFORMATION FOR SEQ ID NO:32:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 165 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear





1	441	MOLECULE	י שעסבי.	CDNA
1	11.	. 1417.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1	LIPLE	CHANA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AGTACTGACA	CAGTCTCCAG	CCACCCTGTC	TTTGTCTCCA	GGGGAAAGAG	CCACCCTCTC	60
CTGCAGGGCC	AGCTCAAGTG	TAAATTACAT	GCACTGGTAC	CAACAGAGAC	CTGGCCAGGC	120
TCCCAGGCTC	CTCATCTATG	CCACTAGTAA	CCTGGCTTCT	GGCAT		165

### (2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 146 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCGCGGGTTA	ATACTCCACT	GCTGACAGTA	ATAAACCGCA	AAATCTTCAG	GCTCTAGACT	60
GCTGATGGTG	AGAGTGAAAT	CTGTCCCAGA	CCCGGATCCA	${\tt CTGAACCTGG}$	CTGGGATGCC	120
AGAAGCCAGG	TTACTAGTGG	CATAGA				146

- (2) INFORMATION FOR SEQ ID NO:34:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 280 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO





- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 2...280
  - (D) OTHER INFORMATION:

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

- A GTA CTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG GAA AGA

  Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg

  1 5 10 15
- GCC ACC CTC TCC TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG CAC TGG
  Ala Thr Leu Ser Cys Arg Ala Ser Ser Val Asn Tyr Met His Trp
  20 25 30
- TAC CAA CAG AGA CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT GCC ACT

  Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ala Thr

  35 40 45
- AGT AAC CTG GCT TCT GGC ATC CCA GCC AGG TTC AGT GGA TCC GGG TCT

  Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser

  50 55 60
- GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTA GAG CCT GAA GAT TTT 241
  Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
  65 70 75 80
- GCG GTT TAT TAC TGT CAG CAG TGG AGT ATT AAC CCG CGG
  Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg
  85 90

# (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 93 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein





- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

 Val
 Leu
 Thr
 Gln
 Ser
 Pro
 Ala
 Thr
 Leu
 Ser
 Leu
 Ser
 Pro
 Gly
 Arg

 Ala
 Thr
 Leu
 Ser
 Cys
 Arg
 Ala
 Ser
 Ser
 Ser
 Val
 Asn
 Tyr
 Met
 His
 Trp

 Ala
 Thr
 Leu
 Ser
 Ser
 Ser
 Ser
 Leu
 Leu
 Ile
 Tyr
 Ala
 Thr

 Asn
 Leu
 Ala
 Ser
 Gly
 Ile
 Pro
 Ala
 Arg
 Phe
 Ser
 Gly
 Ser
 Arg
 Phe
 Ser
 Gly
 Ser
 Arg
 Ile
 Tyr
 Ala
 Tyr
 Ala
 Tyr
 Ala
 Tyr
 Ala
 Arg
 Phe
 Ser
 Gly
 Ile
 Arg
 Ile
 A

- (2) INFORMATION FOR SEQ ID NO:36:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

# TCGAGTACTG ACACAGTCTC CAGCCAC

27

- (2) INFORMATION FOR SEQ ID NO:37:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single





1	ומי)	TOPOLOGY:	linear
1		111111111111111111111111111111111111111	TIMEGI

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

#### GACCGCGGGT TAATACTCCA CTGCTGA

27

### (2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 94 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 27...92
  - (D) OTHER INFORMATION:

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC 53

Met Gly Trp Ser Cys Ile Ile Leu Phe

TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC GAG ATA GTA CT Leu Val Ala Thr Ala Thr Gly Val His Ser Glu Ile Val 10 15 20

94

(2) INFORMATION FOR SEQ ID NO:39:





- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

(2) INFORMATION FOR SEQ ID NO:40:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1 5 10 15

Val His Ser Glu Ile Val
20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GACTGTGTCA GTACTATCTC GGAGTGGACA

30

- (2) INFORMATION FOR SEQ ID NO:41:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 55 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: cDNA



(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:	
GGGCAGCCTC CTAAGTTGCT CATTTACTGG GCGTCGACTA GGGAATCTGG GGTAC	55
(2) INFORMATION FOR SEQ ID NO:42:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 51 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:	
CCCAGATTCC CTAGTCGACG CCCAGTAAAT GAGCAACTTA GGAGGCTGCC C	51
(2) INFORMATION FOR SEQ ID NO:43:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 321 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	

(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(ix) FEATURE:





- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...321
- (D) OTHER INFORMATION: F9HZLC1-0

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAA	АТА	GTA	CTG	ACA	CAG	TCT	CCA	GCC	ACC	CTG	TCT	TTG	тст	CCA	GGG	48
Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	
1				5					10					15		
GAA	AGA	GCC	ACC	CTC	TCC	TGC	AGG	GCC	AGC	TCA	AGT	GTA	AAT	TAC	ATG	96
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	
			20					25					30			
CAC	TICC	መልሮ	$C \Lambda \Lambda$	CAC	AGA	CCT	CCC	CAC	CCT	CCC	A C C	CMC	CITIC	N III C	ma m	144
					Arg											T44
1112	тър	35	GIII	GIII	Arg	PIO	40	GIII	Ala	PIO	Arg		Leu	тте	TYL	
		,,					40					45				
GCC	ACT	AGT	AAC	CTG	GCT	TCT	GGC	ATC	CCA	GCC	AGG	TTC	AGT	GGA	TCC	192
Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	
	50					55					60					
GGG	TCT	GGG	ACA	GAT	TTC	ACT	CTC	ACC	ATC	AGC	AGT	CTA	GAG	CCT	GAA	240
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro	Glu	•
65					70					75					80	
GAT	TTT	GCG	GTT	TAT	TAC	TGT	CAG	CAG	TGG	AGT	ATT	AAC	CCG	CGG	ACG	288
Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ile	Asn	Pro	Arg	Thr	
				85					90					95		
ጣጥረ	CCC	CCA	CCC	7 CC	220	СПС	CAC	A MC	7 7 7	CC 3						201
					AAG											321
rne	стХ	GTĀ		rnr	Lys	val	GIU		гАг	arg						
			100					105								

### (2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 107 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

105



(iii)	HYPOTHETICAL:	NO
\ ~ ~ ~ /	TATE OF HELT LOND.	INC

- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly 5 10 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Asn Tyr Met 20 25 His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr 40 Ala Thr Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser 55 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu 70 75 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr 90 95 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg

# (2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 134 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

100

- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCTGGACAAG GGCTCAAGTG GATGGGATGG ATAAACACCA GAAATGGAAA GTCAACATAT 60 GTTGATGACT TCAAGGGACG GTTTGTCTTC TCTCTAGACT CCTCTGTCAG CACGGCATAT 120 CTACAGATCA GCAG 134

## (2) INFORMATION FOR SEQ ID NO:46:





	(i)	SEQUENCE	CHARACTERISTICS:
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- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGTACCCTGG CCCCAGTAAG TAAAAGGGAA GTAACCATCC ATATTCCCTT CTCTCGTACA 60 GTAATACACT GCAGTGTCGT CAGCCTTTAG GCTGCTGATC TGTAGATATG CCGTGCTGAC 120 AGAGGAGTCT AGAG

### (2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 225 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...225
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CCT GGA CAA GGG CTC AAG TGG ATG GGA TGG ATA AAC ACC AGA AAT GGA
Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile Asn Thr Arg Asn Gly
1 5 10 15





AAG	TCA	ACA	TAT	GTT.	GAT	GAC	TTC	AAG	GGA	CGG	T.I.I.	GTC	TTC	TCT	CTA	96
Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe	Lys	Gly	Arg	Phe	Val	Phe	Ser	Leu	
			20					25					30			
GAC	TCC	TCT	GTC	AGC	ACG	GCA	TAT	CTA	CAG	ATC	AGC	AGC	CTA	AAG	GCT	144
Asp	Ser	Ser	Val	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	
		35					40					45				
GAC	GAC	ACT	GCA-	GTG	TAT	TAC	TGT	ACG	AGA	GAA	GGG	AAT	ATG	GAT	GGT	192
Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Thr	Arg	Glu	Gly	Asn	Met	Asp	Gly	
	50					55					60					
TAC	TTC	CCT	TTT	АСТ	TAC	TGG	GGC	CAG	GGT	ACC						225
Tyr	Phe	Pro	Phe	Thr	Tyr	Trp	Gly	Gln	Gly	Thr						
65					70					75						

- (2) INFORMATION FOR SEQ ID NO:48:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 75 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE: internal
  - (vi) ORIGINAL SOURCE:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

(2) INFORMATION FOR SEQ ID NO:49:

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:
TTTCCTGGAC AAGGGCTCAA GTGGATG
(2) INFORMATION FOR SEQ ID NO:50:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(11)
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:
TTTGGTACCC TGGCCCCAGT AAGT
(2) INFORMATION FOR SEQ ID NO:51:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

27

24

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 27 base pairs

(ii) MOLECULE TYPE: cDNA





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- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...363
  - (D) OTHER INFORMATION: F9HZHC 1-1

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CA	G GI	'G C	AA (	СТА	GTO	G CA	A TC	r ggd	TCT	GAG	TŢC	AAG	AAC	G CC	r ggo	GCC	48
G1	n Va	1 G	ln 1	Leu	Val	. Glı	n Sei	Gl <sub>3</sub>	/ Ser	Glu	Let	ı Lys	Lys	Pro	Gl <sub>y</sub>	/ Ala	-
1					5					10					15		
TC	A GT	G A	AG (	ታጥጥ	ጥሮር	י יייניני	ን አአር		, mcm		<b></b>					TAT	
Se:	r Va	l Ly	s V	Val	Ser	Cvs	Live	Δla	Sor	Clu	TAC	ACC	TTC	: ACI	AAC	TAT Tyr	96
		-		20		012	,y.c	, 1110	25	GIY	TAT	Thr	Pne		Asn	Tyr	
									23					30			
GGZ	TA A	G AA	C I	rgg	GTG	CGA	CAG	GCC	CCT	GGA	CAA	GGG	СТС	AAG	TGG	ATG	144
Gly	/ Me	t As	n I	rp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Lys	Trp	Met	
		35	i					40					45				
CO	, ma																
Cla	· TGO	3 A'I	'A A	AC	ACC	AGA	AAT	GGA	AAG	TCA	ACA	TAT	GTT	GAT	GAC	TTC	192
GLY	50	, 11	е А	sn	rnr	Arg		Gly	Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe	
	50						55					60					
AAG	GG <i>I</i>	CG	G T	$_{ m TT}$	GTC	TTC	тст	СТА	GAC	ጥርር	ጥርጥ	GTC	200	7.00	221		
Lys	G13	Ar	g Pi	he	Val	Phe	Ser	Leu	Asp	Ser	Ser	Val	Sar	Th~	GCA	TAT	240
65						70				201	75	Val	SET	TILL	Ата	1yr 80	
																00	
CTA	CAG	AT	CAC	GC .	AGC	CTA	AAG	GCT	GAC	GAC	ACT	GCA	GTG	ТАТ	TAC	TGT	288
Leu	Gln	. I1	e Se	er	Ser	Leu	Lys	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
					85					90					95		
7.00	202			~~.													
Thr	AGA	GAA	A GC	3G Æ	AAT	ATG	GAT	GGT	TAC	TTC	CCT	TTT	ACT	TAC	TGG	GGC	336
1111	Arg	GI	10 10		Asn	Met	Asp	Gly		Phe	Pro	Phe	Thr	Tyr	Trp	Gly	
			1.0						105					110			
CAG	GGT	ACC	CI	rg d	TC	ACC	GTC	ጥርር	ጥሮል								
							Val										363
		115				-		120									



#### (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 121 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:
- Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala 1 5 10 15
- Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
  20 25 30
- Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Lys Trp Met 35 40 45
- Lys Gly Arg Phe Val Phe Ser Leu Asp Ser Ser Val Ser Thr Ala Tyr
  65 70 75 80
- Leu Gln Ile Ser Ser Leu Lys Ala Asp Asp Thr Ala Val Tyr Tyr Cys
  85 90 95
- Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly
  100 105 110
- Gln Gly Thr Leu Val Thr Val Ser Ser 115 120
- (2) INFORMATION FOR SEQ ID NO:53:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 82 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear





60

82

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:
CAACAGAGAC CTGGCCAGGC TCCCAAGCCC TGGATCTATG CCACGAGTAA CCTGGCTAGC GGCGTCCCAG CCAGGTTCAG TG
(2) INFORMATION FOR SEQ ID NO:54:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO

- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GATCCACTGA ACCTGGCTGG GACGCCGCTA GCCAGGTTAC TCGTGGCATA GATCCAGGGC 60 TTGGGAGCCT GGCCAGGTCT CTGTTGGTAC 90

- (2) INFORMATION FOR SEQ ID NO:55:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 27 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE: internal
  - (vi) ORIGINAL SOURCE:





# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gln	Gln	Arg	Pro	Gly	Gln	Ala	Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr	Ser
1				5					10					15	
Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser					
			20					25							

### (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 321 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...321
  - (D) OTHER INFORMATION: F9HZLC 1-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GAA	ATA	GTA	CTG	ACA	CAG	TCT	CCA	GCC	ACC	CTG	тст	TTG	тст	CCA	GGG	48
Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	
1				5					10					15		
GAA	AGA	GCC	ΔCC	CTC	ጥርር	TOO	700	ccc	7.00	ma.	AGT	a==				
																96
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	
			20					25					30			
CAC	TGG	TAC	CAA	CAG	AGA	CCT	GGC	CAG	GCT	CCC	AAG	CCC	TGG	ATC	TAT	144
His	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ala	Pro	Lys	Pro	Trp	Ile	Tyr	
		35					40					45				
GCC	ACG	AGT	AAC	CTG	GCT	AGC	GGC	GTC	CCA	GCC	AGG	TTC	AGT	GGA	TCC	192
											Arg					
	50					55					60				·	

GGG Gly 65	TCT Ser	GGG Gly	ACA Thr	GAT Asp	TTC Phe 70	ACT Thr	CTC Leu	ACC Thr	ATC Ile	AGC Ser 75	AGT Ser	CTA Leu	GAG Glu	CCT Pro	GAA Glu 80	240
GAT Asp	TTT Phe	GCG Ala	GTT Val	TAT Tyr 85	TAC Tyr	TGT Cys	CAG Gln	CAG Gln	TGG Trp 90	AGT Ser	ATT Ile	AAC Asn	CCG Pro	CGG Arg 95	ACG Thr	288
					AAG Lys											321

105

## (2) INFORMATION FOR SEQ ID NO:57:

100

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 107 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly 1 5 10 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Asn Tyr Met 25 His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Lys Pro Trp Ile Tyr 40 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser 55 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu 70 75 Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr 85 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg 100

(2) INFORMATION FOR SEQ ID NO:58:



41

41

	(ii) MOLECULE TYPE: cDNA
	(iii) HYPOTHETICAL: NO
	(iv) ANTISENSE: NO
	(v) FRAGMENT TYPE:
	(vi) ORIGINAL SOURCE:
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:
	GATCCGGGTC TGGGACAGAT TACACTCTCA CGATATCCAG T
	(2) INFORMATION FOR SEQ ID NO:59:
	(i) SEQUENCE CHARACTERISTICS:
F	(A) LENGTH: 41 base pairs
	(B) TYPE: nucleic acid
<del></del> -	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
not find that	(ii) MOLECULE TYPE: cDNA
- -	(iii) HYPOTHETICAL: NO
	(iv) ANTISENSE: NO
•	(v) FRAGMENT TYPE:
	(vi) ORIGINAL SOURCE:
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:
	CTAGACTGGA TATCGTGAGA GTGTAATCTG TCCCAGACCC G
	(2) INFORMATION FOR SEQ ID NO:60:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 13 amino acids
	(B) TYPE: amino acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 41 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide





(	ĺ.	ii	. )	HYPOTHETICAL	NC

- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser 1 5 10

### (2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 321 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...321
  - (D) OTHER INFORMATION: F9HZLC 1-2

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAA ATA GTA CTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly

1 5 10 15

GAA AGA GCC ACC CTC TCC TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG 96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Asn Tyr Met
20 25 30

CAC TGG TAC CAA CAG AGA CCT GGC CAG GCT CCC AAG CCC TGG ATC TAT

144
His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Lys Pro Trp Ile Tyr

35 40 45



GCC Ala	ACG Thr 50	AGT Ser	AAC Asn	CTG Leu	GCT Ala	AGC Ser	GGC Gly	GTC Val	CCA Pro	GCC Ala	Arg	TTC Phe	AGT Ser	GGA Gly	TCC Ser	192
						<i>J J</i>					60					
GGG	TCT	GGG	ACA	GAT	TAC	ACT	СТС	ACG	АТА	TCC	AGT	СТА	GAG	ССТ	GAA	240
G1y 65	Ser	Gly	Thr	Asp		Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro	Glu	
					70					75					80	
GAT	TTT	GCG	GTT	TAT	TAC	TGT	CAG	CAG	TGG	AGT	ATT	AAC	CCG	CGG	ACG	288
Asp	Phe	Ala	Val		Tyr	Cys	Gln	Gln	Trp	Ser	Ile	Asn	Pro	Arg	Thr	
				85					90					95		
TTC	GGC	GGA	GGG	ACC	AAG	GTG	GAG	ATC	AAA	CGA						321
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg						321
			100					105						•		

# (2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 107 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	011
Glu	Arg	Ala	Thr	Leu	Ser	Cvs	Ara	Ala	Ser	Ser	Sor	17a 1	7 00		M-+
			20				5	25	501	DCI	Set	vai		ıyr	мес
													30		
His	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ala	Pro	Lys	Pro	Trp	Ile	Tvr
		35					40						~		-1 -
												45			
Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arq	Phe	Ser	Glv	Ser
	50					55							~	011	DCI
											60				
Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro	Glu
65					70										
										75					80
Asp	Phe	Ala	Val	ጥህን	ጥኒያ	Cvc	C1n	C1-	m	<b>~</b> -	~ 7	_	_		
-				~ 1 ~	Tyr	Cys	GIII	GIII	ттр	ser	тте	Asn	Pro	Arg	Thr
				85					90					95	
														90	





Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
			100					105		

(2)	INFORMATION	FOR	SEO	TD	NO · 63
· — /	TTIL OTHER TENT	LOIL	עבים	$\perp \nu$	140.00

(i) SEQUENCE	CHARACTERISTICS:
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- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

AGTACTCACC CAGAGCCCAA GCAGCCTGAG CGCCAGCGTG GGTGACAGAG TGACCATCAC 60
CTGCAGGGCC AGCTCAAGTG TAAATTACAT GCACTGGTAC CAGCAGAAGC CAGGTAAGGC 120
TCCAAAGCCT TGGATCTACG CCACTAGTAA CCTGGCTTCT GGTGT 165

## (2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 161 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CCGCGGGTTA	ATACTCCACT	GCTGGCAGTA	GTAGGTGGCG	ATATCCTCTG	GCTGGAGGCT	60
GCTGATGGTG	${\tt AAGGTGTAGT}$	${\tt CTGTACCGCT}$	ACCGGATCCG	CTGAATCTGC	TTGGCACACC	120
AGAAGCCAGG	TTACTAGTGG	CGTAGATCCA	AGGCTTTGGA	G		161

## (2) INFORMATION FOR SEQ ID NO:65:



(i)	SEQUENCE	CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 2...280
  - (D) OTHER INFORMATION:

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

A GTA CTC ACC CAG AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT GAC AG  Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Ar  1 5 10 15	A 49
GTG ACC ATC ACC TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG CAC TGG Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met His Trp 20 25 30	97
TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG CCT TGG ATC TAC GCC ACT Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr Ala Thr 35 40 45	145
AGT AAC CTG GCT TCT GGT GTG CCA AGC AGA TTC AGC GGA TCC GGT AGC Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser 50 55 60	193
GGT ACA GAC TAC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAT ATC Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile 70 75 80	241
GCC ACC TAC TAC TGC CAG CAG TGG AGT ATT AAC CCG CGG Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg 85 90	280



# (2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 93 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

1 5 10 15

Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met His Trp 20 25 30

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr Ala Thr 35 40 45

Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser 50 55 60

Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile
65 70 75 80

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg 85 90

# (2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:





(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:	
TTTAGTACTC ACCCAGAGCC CAAGCAG	27
(2) INFORMATION FOR SEQ ID NO:68:	_,
1 1 5 <u>1</u> 10.00.	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 27 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:	
TTCCGCGGGT TAATACTCCA CTGCTGG	27
(2) INFORMATION FOR SEQ ID NO:69:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 33 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	
CTCGAGCAGT ACTATCTGGG AGTGGACACC TGT	33

- 10
- (i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:70:

(A) LENGTH: 17 amino acids





- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:71:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 48 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGACGTTCGG CCAAGGGACC AAGGTGGAAA TCAAACGGAC TGTGGCGG

- (2) INFORMATION FOR SEQ ID NO:72:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO





1	(is	7	Δ1	TTT .	TCI	באזכ	F: •	NO

- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CGCCGCCACA GTCCGTTTGA TTTCCACCTT GGTCCCTTGG CCGAACGTCC GC

52

#### (2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 321 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...321
  - (D) OTHER INFORMATION: F9HZLC 2-0

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAG ATA GTA CTC ACC CAG AGC CCA AGC CTG AGC CTG AGC GCC AGC GTG GGT

Gln Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 10 15

GAC AGA GTG ACC ATC ACC TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG 96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met
20 25 30

CAC TGG TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG CCT TGG ATC TAC

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr

35 40 45

GCC ACT AGT AAC CTG GCT TCT GGT GTG CCA AGC AGA TTC AGC GGA TCC 192
Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser

50 60

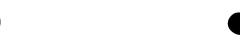
GGT	AGC	GGT	ACA	GAC	TAC	ACC	TTC	ACC	ATC	AGC	AGC	CTC	CAG	CCA	GAG	240
Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Phe	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	
65					70					75					80	

GAT ATC GCC ACC TAC TGC CAG CAG TGG AGT ATT AAC CCG CGG ACG 288 Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr 85 90 95

TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGG 321 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg 100

#### (2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 107 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:
- Gln Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly 10
- Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met 20 25 30
- His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr 40
- Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser 55
- Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu 65 70 75
- Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr 85 90
- Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg



# (2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 94 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 27...94
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC 53

Met Gly Trp Ser Cys Ile Ile Leu Phe 5

94

TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC CAG ATA GTA CT Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Ile Val Leu 10 15 20

- (2) INFORMATION FOR SEQ ID NO:76:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal





(vi) ORIGINAL	SOURCE:
---------------	---------

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly 1 5 5 10 10 15 15 Val His Ser Gln Ile Val Leu 20

## (2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 401 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 27...401
  - (D) OTHER INFORMATION: F9HZLC 1-3

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC 53

Met Gly Trp Ser Cys Ile Ile Leu Phe 5

TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC CAG ATA GTA CTG ACA CAG

Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Ile Val Leu Thr Gln

10 25

TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC

Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser

30 35 40

TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG CAC TGG TAC CAA CAG AGA 197





Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	His	Trp	Tyr	Gln	Gln	Arg
			45					50					55		

CCT GGC CAG GCT CCC AAG CCC TGG ATC TAT GCC ACG AGT AAC CTG GCT

Pro Gly Gln Ala Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala

60 65 70

AGC GGC GTC CCA GCC AGG TTC AGT GGA TCC GGG TCT GGG ACA GAT TAC 293

Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr

75 80 85

ACT CTC ACG ATA TCC AGT CTA GAG CCT GAA GAT TTT GCG GTT TAT TAC

Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr

90 95 100 105

TGT CAG CAG TGG AGT ATT AAC CCG CGG ACG TTC GGC GGA GGG ACC AAG

Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr Phe Gly Gly Gly Thr Lys

110 115 120

GTG GAG ATC AAA

Val Glu Ile Lys

125

- (2) INFORMATION FOR SEQ ID NO:78:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 125 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE: internal
  - (vi) ORIGINAL SOURCE:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1 5 10 15

Val His Ser Gln Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu
20 25 30

Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val

		35					40					45			
Asn	Tyr	Met	His	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ala	Pro	Lys	Pro
	50					55					60				
Trp	Ile	Tyr	Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe
65					70					75					80
Ser	${\tt Gly}$	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Let
				85					90					95	
Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ile	Ası
			100					105					110		
Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys			
		115					120					125			

- (2) INFORMATION FOR SEQ ID NO:79:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 81 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGGCCTCTGG ATACACCTTC ACTAACTATG GAATGAACTG GGTGCGACAG GCCCCTGGAC AAGGGCTCGA GTGGATGGGA T

60

- (2) INFORMATION FOR SEQ ID NO:80:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 99 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:





60

99

86

(xi)	SEOUENCE	DESCRIPTION:	SEO	ID	NO:80:
------	----------	--------------	-----	----	--------

TGGTGTTTAT CCATCCCATC CACTCGAGCC CTTGTCCAG

TGTCTAGAGA GAAGACAAAC CGTCCCTTGA AGTCATCAAC ATATGTTGAC TTTCCATTTC

(2) INFORMATION FOR SEQ ID NO:81:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 87 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:	
GGTTTGTCTT CTCTCTAGAC ACCTCTGTCA GCACGGCATA TCTACAGATC AGCAGCCTAA	60
AGGCTGAGGA CACTGCAGTG TATTTCT	87
(2) INFORMATION FOR SEQ ID NO:82:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 86 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:	
GGTACCCTGG CCCCAGTAAG TAAAAGGGAA GTAACCATCC ATATTCCCTT CTCTCGTACA	60

GAAATACACT GCAGTGTCCT CAGCCT



#### (2) INFORMATION FOR SEQ ID NO:83:

1	' i '	SECUENCE	CHARACTERISTICS:
١	\ <del>-</del> .	PECOPIACE	CHARACTERISTICS

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 3...278
  - (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

AG	GCC	TCT	GGA	TAC	ACC	TTC	ACT	AAC	TAT	GGA	ATG	AAC	TGG	GTG	CGA	47
	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	Gly	Met	Asn	Trp	Val	Arg	
	1				5					10					15	
CAG	GCC	CCI	GGA	CAA	GGG	CTC	GAG	TGG	ATG	GGA	TGG	ATA	AAC	ACC	AGA	95
Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Trp	Ile	Asn	Thr	Arg	
				20					25					30	_	
AAT	GGA	AAG	TCA	ACA	TAT	GTT	GAT	GAC	TTC	AAG	GGA	CGG	TTT	GTC	TTC	143
Asn	Gly	Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe	Lys	Gly	Arg	Phe	Val	Phe	
			35					40					45			
TCT	CTA	GAC	ACC	TCT	GTC	AGC	ACG	GCA	TAT	СТА	CAG	ATC	AGC	AGC	СТА	191
															Leu	
		50					55					60				
AAG	GCT	GAG	GAC	ACT	GCA	GTG	TAT	TTC	TGT	ACG	AGA	GAA	GGG	AAT	ATG	239
			Asp													
	65					70			_		75		_			

278

GAT GGT TAC TTC CCT TTT ACT TAC TGG GGC CAG GGT ACC

Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr

80



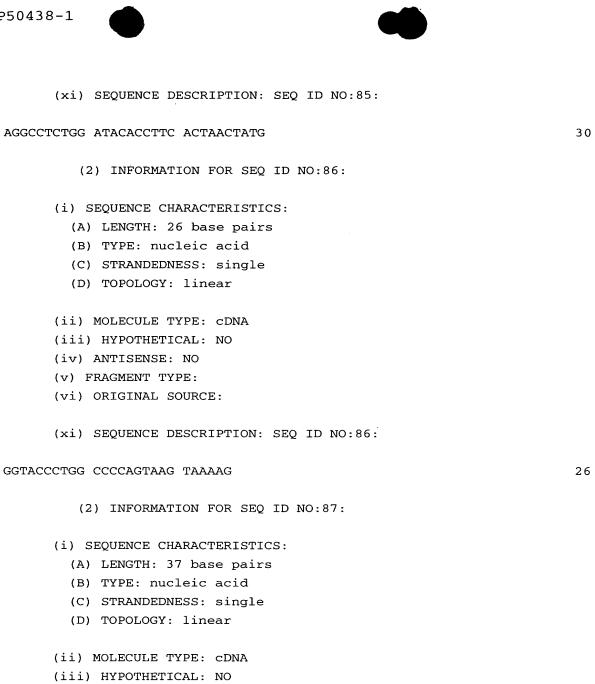
### (2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 92 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:
- Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Arg Gln

  1 5 10 15
- Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Arg Asn
  20 25 30
- Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg Phe Val Phe Ser 35 40 45
- Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys 50 55 60
- Ala Glu Asp Thr Ala Val Tyr Phe Cys Thr Arg Glu Gly Asn Met Asp 65 70 75 80
- Gly Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr 85 90

## (2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:



- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

#### CCAGACTCGA CTAGTTGGAT CTGGGAGTGG ACACCTG

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:





(	A)	LENGTH:	446	base	pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 27...446
  - (D) OTHER INFORMATION: F9HZHC 3-0

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GAA	TTCT	GAG	CACA	CAGG.	AC C	TCAC									C TTC u Phe	53
								C OI.	y 11.	p se		2 II	e II	е пе	u Pne	
							1				5					
ጥጥር	СПУ	GCA	ልሮአ	CCT	202	CCM	CMC	CAC	maa	a va	3.000	<b>~~</b>	C.T. 1	~~~	CAA	
																101
	vai	Ата	THE	Ala		GIY	vaı	HIS	Ser	GIn	He	Gln	Leu	Val	Gln	
10					15					20					25	
TCT	GGG	TCT	GAG	TTG	AAG	AAG	CCT	GGG	GCC	TCA	GTG	AAG	GTT	TCC	TGC	149
Ser	Gly	Ser	Glu	Leu	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	
				30					35					40		
AAG	GCC	тст	GGA	TAC	ACC	TTC	АСТ	AAC	TAT	GGA	ATG	AAC	TGG	GTG	CGA	197
Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	Gly	Met	Asn	Trp	Val	Ara	
			45					50		_			55		3	
													33			
CAG	GCC	CCT	GGA	CAA	GGG	CTC	GAG	TGG	ATG	GGA	TGG	АТА	AAC	ACC	AGA	245
								Trp								243
		60	1	022		Dea	65	110	1100	Сту	тър		ASII	TIIT	AIG	
		00					0.5					70				
	~~-															
								GAC								293
Asn	Gly	Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe	Lys	Gly	Arg	Phe	Val	Phe	
	75					80					85					

TCT CTA GAC ACC TCT GTC AGC ACG GCA TAT CTA CAG ATC AGC AGC CTA

Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu 90 95 100 105

AAG GCT GAG GAC ACT GCA GTG TAT TTC TGT ACG AGA GAA GGG AAT ATG

Lys Ala Glu Asp Thr Ala Val Tyr Phe Cys Thr Arg Glu Gly Asn Met

110 115 120

GAT GGT TAC TTC CCT TTT ACT TAC TGG GGC CAG GGT ACC CTG GTC ACC

Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr

125

130

135

GTC TCC TCT

Val Ser Ser

140

- (2) INFORMATION FOR SEQ ID NO:89:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 140 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE: internal
  - (vi) ORIGINAL SOURCE:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:



7	

		100					105					110				
Tyr E	Phe Cys	Thr	Arg	Glu	Gly	Asn	Met	Asp	Gly	Tyr	Phe	Pro	Phe	Thr		
	115					120					125					
Tyr 1	rp Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser						
1	130				135					140						
(2) IN	FORMAT:	ION F	OR S	SEQ ]	D NO	90:90	:									
	(i) SI															
		LENG					rs									
		TYPE														
		STRA					9									
	(D)	TOPO	)LOG Y	(: 11	.near	:										
	(ii) N	MOLEC	THE	ΨΥΡΕ	· cr	ΔΜ										
	(iii)															
	(iv) A															
	(v) FF															
	(vi) (															
	(xi) S	EQUE	NCE	DESC	RIPT	'ION:	SEÇ	ID	NO:9	0:						
	TGACA C							ATCI	GTT	GGGG	ACAG	AG T	CACC	ATCA	2	60
TTGCA	GGGCC A	GCTC	AAGT	'G TA	AATT	ACAT	1									90
	(0)															
	(2)	INF	ORMA	TTON	FOR	SEQ	ID	NO:9	1:							
	(i) SE	OUEN	CE C	HARA	СФЕВ	て マ ア エ	CS.									
		LENG														
		TYPE				_										
		STRA														
		TOPO														
											-					
	(ii) M	OLEC	ULE '	TYPE	: cD	NA										
	(iii)	HYPO	THET	ICAL	: NO											
	(iv) A	NTIS	ENSE	: NO												
	(v) FR	AGMEI	NT T	YPE:												
	(vi) 0	RIGI	NAL ;	SOUR	CE:											
	(xi) S	EQUE	NCE I	DESC	RIPT	ION:	SEQ	ID 1	NO:9	1:						
		00001	7m v ~ :	2 62 6				~~-								
CTTGAT	rggga c	GCCG(	_TAG(	CAC	G'PTZ	ACTC	GTG	GCAT.	AGA :	rcca(	GGGC'	rt G	GGAG	CTTTG	į	60

108

CCAGGTTTCT GTTGGTACCA GTGCATGTAA TTTACACTTG AGCTGGCC





#### (2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE	CHARACTERISTICS:
--------------	------------------

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TAACCTGGCT AGCGGCGTCC CATCAAGGTT CAGTGGATCC GGGTCTGGGA CAGATTACAC

TCTCACGATA TCCAGTCTAC AACCTGAAGA TTTTGCGACT TATTACTG

108

- (2) INFORMATION FOR SEQ ID NO:93:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 102 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGCGCCGCCA CAGTTCGTTT GATCTCCAGC TTGGTCCCTC CGCCGAACGT CCGCGGGTTA 60
ATACTCCACT GCTGACAGTA ATAAGTCGCA AAATCTTCAG GT 102

- (2) INFORMATION FOR SEQ ID NO:94:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 330 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single





# (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 2...328
  - (D) OTHER INFORMATION:

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Α (	GTA (	CTG .	ACA	CAG	TCT (	CCA	TCC	TCC	CTG '	ጥርጥ	GC A	ጥርጥ ፣	стт ,	200	GAC AG	
7	/al 1	Leu '	Thr	Gln .	Ser :	Pro	Ser	Ser	Leu :	Ser	Ala	Ser 1	(7a) (	30G (	asp Ar	A 49
	1				5					10		DCI	vai (		asp ar 15	g
GTC Val	ACC	C ATO	C AC ⇒ Thi 20	r TG(	C AGO	G GC0	C AGO	C TC	A AG	r GT	A AA	T TAC	C ATO	G CAC	C TGG s Trp	97
TAC Tyr	CAA Gln	CAC Glr 35	AAA Lys	A CCT	GGC Gly	AA/	A GCT 3 Ala 40	CCC Pro	C AAG D Lys	G CCC	TG(	G ATO 11e 45	TAT	GCC Ala	ACG Thr	145
AGT Ser	AAC Asn 50	CTG Leu	GCT Ala	'AGC	GGC Gly	GTC Val 55	Pro	TCA Ser	AGG Arg	TTC Phe	AGT Ser	GGA Gly	TCC Ser	GGG Gly	TCT	193
GGG Gly 65	ACA Thr	GAT Asp	TAC Tyr	ACT Thr	CTC Leu 70	ACG Thr	ATA Ile	TCC Ser	AGT Ser	CTA Leu 75	CAA Gln	CCT Pro	GAA Glu	GAT Asp	TTT Phe 80	241
GCG Ala	ACT Thr	ТАТ Туг	TAC Tyr	TGT Cys 85	CAG Gln	CAG Gln	TGG Trp	AGT Ser	ATT Ile 90	AAC Asn	CCG Pro	CGG Arg	ACG Thr	TTC Phe 95	GGC Gly	289
GGA Gly	GGG Gly	ACC Thr	AAG Lys 100	CTG Leu	GAG Glu	ATC Ile	AAA Lys	CGA Arg 105	ACT Thr	GTG Val	GCG Ala	GCG Ala	CC			330



### (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg

1 10 15

Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met His Trp
20 25 30

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr Ala Thr
35 40 45

Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser 50 55 60

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe 65 70 75 80

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr Phe Gly 85 90 95

Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala 100 105

#### (2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:



(vi) ORIGINAL SOUR	RCE
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(xi	) SEQUENCE	DESCRIPTION:	SEO	ID	NO:96:
-----	------------	--------------	-----	----	--------

## CAAGTACTGA CACAGTCTCC ATCCTC

26

## (2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

## AGGGCGCCGC CACAGTTCGT TTGATC

26

## (2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 412 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 27...412
  - (D) OTHER INFORMATION: F9HZLC 3-0





# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GAA	TTCT	GAG	CACA	CAGG	AC C	TCAC	C AT	G GG	A TG	G AG	С ТС	T AT	'C A'I	C CI	C TTC	53
							M∈	t Gl	y Tr	p Se	er Cy	s Il	e Il	e Le	u Phe	
							1				5					
ТТС	GTA	GCA	ACA	GCI	ACA	GGT	GTC	CAC	TCC	CAG	ATA	GTA	СТС	ACA	CAG	101
															Gln	
10					15					20					25	
TCT	CCA	TCC	TCC	CTG	TCT	GCA	TCT	GTT	GGG	GAC	AGA	GTC	ACC	ATC	ACT	149
															Thr	
				30					35		_			40		
TGC	AGG	GCC	AGC	TCA	AGT	GTA	AAT	TAC	ATG	CAC	TGG	TAC	CAA	CAG	AAA	197
											Trp					
			45					50			0	-	55		•	
CCT	GGC	AAA	GCT	CCC	AAG	CCC	TGG	ATC	TAT	GCC	ACG	AGT	AAC	CTG	GCT	245
Pro	Gly	Lys	Ala	Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr	Ser	Asn	Leu	Ala	
		60					65					70				
AGC	GGC	GTC	CCA	TCA	AGG	TTC	AGT	GGA	TCC	GGG	TCT	GGG	ACA	GAT	TAC	293
Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	
	75					80					85					
											TTT					341
Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	
90					95					100					105	
rgt	CAG	CAG	TGG	AGT	ATT	AAC	CCG	CGG	ACG	TTC	GGC	GGA	GGG	ACC	AAG	389
Cys	Gln	Gln	Trp	Ser	Ile	Asn	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys	
				110					115					120		
CTG	GAG	ATC	AAA	CGA	ACT	GTG	GC									412
Leu	Glu	Ile	Lys	Arg	Thr	Val	Val									

# (2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 129 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single





- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly 10 Val His Ser Gln Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala 20 25 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val 40 Asn Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro 55 Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe 70 75 Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu 90 Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn 105 110 Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val 115 120 125 Val

- (2) INFORMATION FOR SEQ ID NO:100:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:



#### CAAATAGTAC TCTCCCAGTC TCCAGC

- (2) INFORMATION FOR SEQ ID NO:101:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

## GGATAAGCTT GGCGCCGCAA CAGTCGGTTT GATTTCCAGC T

41

- (2) INFORMATION FOR SEQ ID NO:102:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 335 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...335
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CAG ATA GTA CTC TCC CAG TCT CCA GCA ATC CTG TCT GCA TCT CCA GGG Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly

1				5		•	10			15	
					ACT Thr						96
					AAG Lys						144
					GCT Ala						192
	Ser	Gly	Thr		TAC Tyr 70						240

GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG AGT ATT AAC CCA CGG ACG
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr
85 90 95

TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA CGG ACT GTT GCG GCG CC 335

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

#### (2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
1 5 10 15



4	

Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met
			20					25					30		
His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr
		35					40					45			
Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Arg	Val	Glu	Ala	Glu
65					70					75					80
Asp	Ala	Ala	Thr	Tyr	Tyr	Суѕ	Gln	Gln	Trp	Ser	Ile	Asn	Pro	Arg	Thr
				85					90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro
			100					105					110		

## (2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 318 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...318
  - (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CAG	ATA	GTA	CTC	TCC	CAG	TCT	CCA	GCA	ATC	CTG	TCT	GCA	TCT	CCA	GGG	48	
Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile	Leu	Ser	Ala	Ser	Pro	Gly		
1				5					10					15			
GAG	AAG	GTC	ACA	ATG	ACT	TGC	AGG	GCC	AGC	TCA	AGT	GTA	ААТ	TAC	ATG	96	
Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met		
			20					25					30				
CAC	TGG	TAC	CAG	CAG	AAG	CCA	GGA	TCC	TCC	CCC	AAA	CCC	TGG	ATT	TAT	144	



His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr 35 40 45

GCC ACA TCC AAC CTG GCT TCT GGA GTC CCT GCT CGC TTC AGT GGC AGT

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser

50 55 60

GGG TCT GGG ACC TCT TAC TCT CTC ACA ATC AGC AGA GTG GAG GCT GAA 240
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65 70 75 80

GAT GCT GCC ACT TAT TAC TGC CAG CAG TGG AGT ATT AAC CCA CGG ACG

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr

85

90

95

318

TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA
Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

#### (2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 106 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:



-4	

65					70					75					80
Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ile	Asn	Pro	Arg	Thr
				85					90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys						
			100					105							

- (2) INFORMATION FOR SEQ ID NO:106:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

## CAGATCCAAC TAGTGCAGTC TGGACCTGAG

30

- (2) INFORMATION FOR SEQ ID NO:107:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

# TTAAGCTTGC TAGCTGCAGA GACAGTGACC AG

32

(2) INFORMATION FOR SEQ ID NO:108:





(i	) SEOUENCE	CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...369
  - (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CAG	ATC	CAA	CTA	GTG	CAG	TCT	GGA	CCT	GAG	CTG	AAG	AAG	CCT	GGA	GAG	48
Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Leu	Lys	Lys	Pro	Gly	Glu	
1				5					10					15		
ACA	GTC	AAG	ATC	TCC	TGC	AAG	GCT	TCT	GGG	TAC	ACC	TTC	ACA	AAC	TAT	96
Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	
			20					25					30			
GGA	ATG	AAC	TGG	GTG	AAG	CAG	GCT	CCA	GGA	AAG	GGT	TTA	AAG	TGG	ATG	144
Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Lys	Trp	Met	
		35					40					45				
								AAG								192
Gly		Ile	Asn	Thr	Arg	Asn	Gly	Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe	
	50					55					60					
								GAA								240
	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Ser	Ser	Ala	Ser	Thr	Ala	Asn	
65					70					75					80	
								GAG								288
Leu	Gln	Ile	Asp	Asn	Leu	Lys	Asp	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	
				85					90					95		



369

ACA AGA GAA GGG AAT ATG GAT GGT TAC TTC CCT TTT ACT TAC TGG GGC 336

Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly

100 105 110

CAA GGG ACT CTG GTC ACT GTC TCT GCA GCT AGC
Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser
115 120

### (2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 123 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu

1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr 20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met 35 40 45

Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe 50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Ser Ser Ala Ser Thr Ala Asn 65 70 75 80

Leu Gln Ile Asp Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys 85 90 95

Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser 115 120

- (2) INFORMATION FOR SEQ ID NO:110:
- (i) SEQUENCE CHARACTERISTICS:





(A) LENGTH: 363 base pai:	rs
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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...363
  - (D) OTHER INFORMATION:

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CAG	ATC	CAA	CTA	GTG	CAG	TCT	GGA	CCT	GAG	CTG	AAG	AAG	CCT	GGA	GAG	48
Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Leu	Lys	Lys	Pro	Gly	Glu	
1				5					10					15		
ACA	GTC	AAG	ATC	TCC	ŤGC	AAG	GCT	TCT	GGG	TAC	ACC	TTC	ACA	AAC	TAT	96
Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	
			20					25					30			
												TTA				144
Gly	Met		Trp	Val	Lys	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Lys	Trp	Met	
		35					40					45				
												GTT				192
Gly		Ile	Asn	Thr	Arg	Asn	Gly	Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe	
	50					55					60					
												AGC				240
	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Ser	Ser	Ala	Ser	Thr	Ala	Asn	
65					70					75					80	
TTG	CAG	ATC	GAC	AAC	CTC	AAA	GAT	GAG	GAC	ACG	GCT	ACA	TAT	TTC	TGT	288
Leu	Gln	Ile	Asp	Asn	Leu	Lys	Asp	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	
				85					90					95		
ACA	AGA	GAA	GGG	AAT	ATG	GAT	GGT	TAC	TTC	CCT	TTT	ACT	TAC	TGG	GGC	336

Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly
100 105 110

CAA GGG ACT CTG GTC ACT GTC TCT GCA
Gln Gly Thr Leu Val Thr Val Ser Ala
115 120

363

# (2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 121 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

115

- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu 1 5 10 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met 40 Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe 55 Lys Gly Arg Phe Ala Phe Ser Leu Glu Ser Ser Ala Ser Thr Ala Asn 70. 75 Leu Gln Ile Asp Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys 85 90 Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly 100 Gln Gly Thr Leu Val Thr Val Ser Ala